GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 3, 2005, 21:37:29; Search time 52.7808 Seconds (without alignments) 291.060 Million cell updates/sec \$ 100 mm

Title: Perfect score: 09782816-1-22 138

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 1 EVEKIKTTVKESATEBKLTPVILJAKOLAAL 30
BLOSUM62 5,022

1612378 seqs, 512079187 residues

Searched:

Total number of hits satisfying chosen parameters:

1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

. 31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	ហ	4	ω	N	–	No.	Regult
51	51	51	51	51	51	51	51	51	51	52	52	52	52	53	53	53	53	54	54	54	54	56	89	92	109	114	114	135	135		Score	
37.0	37.0	37.0	37.0	37.0	37.0	37.0	37.0	٠	37.0	37.7	37.7	37.7	37.7	38.4	38.4	38.4	38.4	39.1	39.1	39.1	39.1	40.6	64.5	66.7	79.0	82.6	82.6	97.8	97.8	100.0	음	Query
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Q8L0P1	Q8L0P0	Q8L0N9	Q8L0N6	Q8L0N4	Q8KHB8	Q6UYC7	Q8PSI8	Q25636	Q8TZZ5	Q7RT55	Q6FAP3	Q81DX2	Q738U0	001787	Q75CZ5	Q6CF32	Q6BFZ2	GLND_AZOBR	Q6BPD3	C72Y ARATH	Q72JL4	Q874E7	Q9PTG6	Q7T3H1	Q66J30	Q6IRB3	Q7ZXY2	Q6AYH5	DCT2_MOUSE	DCT2_HUMAN	ID	
Q810p1 helicobacte			helicobact		helicobact						acinetoba	bacillus c	bacillus c	caenor	ashbya go		Q6bfz2 paramecium	azospirill		т.	thermus th	paecilomyc		Q7t3h1 brachydanio		xenopus	xenopus	Q6ayh5 rattus norv)8 mus m	Q13561 homo sapien	₽	

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ຫັ	51	37.0	500	-	C72V ARATH	Q9lip6 arabidopsis
2	51	37.0	757	N	Q96WÜ0	
7	51	37.0	770	N	Q72F42	N
8	51	37.0	773	j	GYRB_HELPJ	Q9zlx3 helicobacte
õ	51	37.0	928	N	Q660 <u>B</u> 1	Q660el borrelia
5	51	37.0	932	N	051674	051674 borrelia
F	51	37.0	964	μ	IF2 CHRVO	Q7ny13 chromobacte
ັນ	51	37.0	10917	N	Q93NW6	Q93nw6 streptomyce
Ü	50.5	36.6	213	μ	LIPB SALTI	Q8z8i2 salmonel
4.	50.5	36.6	213	Н	LIPB SALTY	Q8zr03 salmonell
'n	50.5	36.6	380	N	Q7MPUS	Q7mpu5 vibrio vuln

ALIGNMENTS

TISSUE=Platelet;

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RESULT
DCT2_MC
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Best Local S
Matches 30
                                                        28-FEB-2003 (Rel. 41, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Dynactin complex 50 kDs subunit (50 kDs dynein-associated polypeptide)
(p50 dynamitin) (DCTN-50) (Dynactin 2) (Growth cone membrane protein
                                                                                                                        DCT2 MOUSE
Q99KJ8;
28-FEB-2003
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; NCBI_TaxID=10090;
                                     Mus musculus (Mouse)
                                                                                                                                                               MOUSE
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CONFLICT
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                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                           Coiled coil;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictiuse by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Exploring proteomes and analyzing protein processing by mass spectrometric identification of sorted N-terminal peptides.", Nat. Biotechnol. 21:566-569(2003)
                                                                                                                                                                                                              115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Modulates cytoplasmic dynein binding to an organelle, and plays a role in prometaphase chromosome alignment and spindle organization during mitosis. May play a role in synapse formation during brain development.

SUBUNIT: Subunit of dynactin, a multiprotein complex associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
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                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                   EVEKÍKTTVKESATEEKLTPVLLAKOLAAL 144
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als M., Martens L., Van Damme J., Sta
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Coiled coil
Coiled coil
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Pred. No. 1.8e-09;
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Query Match Best Local S Matches 29

Similarity 29; Conserv

97.8**%**; 96.7**%**; 43985

Score 135; DB 1;] Pred. No. 4.5e-09; 1; Mismatches 0;

Length 401;

<u>,</u>

Gaps

<u>,</u>

Conservative

SEQUENCE

DOMAIN

Coiled

PF04912; Dynamitin; 1.

IPR006996;

Dynamitin.

Microtubule;

Cytoskeleton; Direct protein sequencing; Dynein,

Motor protein.

By similarity.
Coiled coil (Potential).
Coiled coil (Potential).
Coiled coil (Potential).
Solution (Potential).

MGD;

#GI:107733; Dctn2.

(See http://www.isb-sib.ch/announce/

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RA Strausberg R.L., Feingold B.A., Grouse L.H., Dérge J.G.,
RA Klauener R.D., Collins F.S., Wagner I., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh R.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Paltey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
RT "Generation and initial analysis of more than 15,000 full-length human
                                                                           This SWISS-PROT entry is copyright. It is product the Entry is copyright. It is copyright.
entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21376052; PubMed=11483508; DOI=10.1093/emboj/20.15.4041; Hoogenraad C.C., Akhmanova A., Howell S.A., Dortland B.R., de Zeeuw C.I., Willemsen R., Visser P., Grosveld F., Galjart N.; "Mammallan Golgi-associated Bicaudal-D2 functions in the dynein-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97289622; PubMed=9144527; DOI=10.1006/bbrc.1997.6447; Abe T.K., Tanaka H., Iwanaga T., Odani S., Kuwano R.; "The presence of the 50-kDa subunit of dynactin complex in the growth cone.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERACTION WITH BICD2.
MEDLINE=21376052; PubMed=11483508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 65-74; 77-91; 102-116; 156-170; 194-216 SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Modulates Cytoplasmic dynein binding to an organelle, and plays a role in prometaphase chromosome alignment and spindl organization during mitosis. May play a role in synapse formatic during brain development.

SUBUNIT: Subunit of dynactin, a multiprotein complex associated with dynein (By similarity). Interacts with BICD2.

SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated. STAGE: present at high levels in both cytoplasmic and membrane-associated forms in neonates. Levels of membrane-associated forms in neonates.
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